

IN THE SPECIFICATION

Please amend the paragraph beginning on page 31, lines 11-31 with the following amended paragraph:

Specifically, Basic Alignment Search Tool (BLAST) (~~www.ncbi.nlm.nih.gov~~) (Altschul et al., 1990, J. of Molec. Biol., 215:403-410, "The BLAST Algorithm; Altschul et al., 1997, Nuc. Acids Res. 25:3389-3402) is a heuristic search algorithm tailored to searching for sequence similarity which ascribes significance using the statistical methods of Karlin and Altschul 1990, Proc. Natl Acad. Sci. USA, 87:2264-68; 1993, Proc. Nat'l Acad. Sci. USA 90: 5873-77. Five specific BLAST programs perform the following tasks: 1) the BLASTP program compares an amino acid query sequence against a protein sequence database; 2) the BLASTN program compares a nucleotide query sequence against a nucleotide sequence database; 3) the BLASTX program compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database; 4) the TBLASTN program compares a protein query sequence against a nucleotide sequence database translated in all six reading frames (both strands); 5) the TBLASTX program compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

Please amend the paragraph beginning on page 31, lines 32-35 with the following amended paragraph:

Smith-Waterman (database: European Bioinformatics Institute ~~www.ebi.ac.uk/bi-sw/~~) (Smith-Waterman, 1981, J. of Molec. Biol., 147:195-197) is a mathematically rigorous algorithm for sequence alignments.

Please amend the paragraph beginning on page 31, lines 36-37 and continuing on page 32, lines 1-5 with the following amended paragraph:

FASTA (see Pearson et al., 1988, Proc. Nat'l Acad. Sci. USA, 85:2444-2448) is a heuristic approximation to the Smith-Waterman algorithm. For a general discussion of the procedure and benefits of the BLAST, Smith-Waterman and FASTA algorithms see Nicolas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.pse.edu) and references cited therein.

Please amend the paragraph beginning on page 45, lines 31-37 and continuing on page 46, lines 1-4 with the following amended paragraph:

The amino acid sequences of S2C6 VL, S2C6 VH and the CDRs of both the VL and VH were submitted for BLASTP searches on April 21, 1999 using both the NR database (All non-redundant GenBank CDS translations+PDS+SwissProt+PIR+PRF) and the Kabat database (Kabat's database of sequences of immunological interest). The sequences found using the NR database can be retrieved using the Accession number at <http://www.ncbi.nlm.nih.gov>. The sequences found using the Kabat database can be retrieved using the Accession number at <http://immune.bme.nwu.edu/database.html> and SEQHUNTII. The results of these searches are shown below: